

Abstract

A method and tools for the biochemical processing of protein samples towards their analysis and identification by, for example, mass spectrometry (MS). The method involves the reversible (non-covalent) immobilization, purification and concentration of proteins onto a solid surface and subsequent solid-phase enzyme-catalyzed proteolysis of the proteins. The constituent peptides are recovered in near-quantitative yields in a format ideally suited for identification by routine MS technologies. The process is easily adapted such that additional chemical and/or enzymatic transformation(s) of the immobilized proteins or peptides can be performed to facilitate the acquisition of and increase the information content obtained from the MS analysis.